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\* EMBnet News bulletin of 04-Dec-2009 \*  
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Dear Users,

Courses in 2010  
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We will organise several courses in 2010 in collaboration with the 3e cycle romand in Biological Sciences:

- 1) Geneva January 25 - 29: Introduction to Statistics for Biologists
- 2) Geneva September 13 - 17: Computational Analysis of Ultra-High-Throughput (UHT) Sequencing Data

#### 1) Introduction to Statistics for Biologists

The course is designed to provide graduate students in the biomedical sciences with experience in the application of basic statistical analysis techniques to a variety of biological problems.

Attendees will work through short tutorials on the topics discussed in the class. During the practical exercises students will learn how to work with the widely used "R" language and environment for statistical computing and graphics.

The course participants are also strongly encouraged to submit in advance (until 09 Jan 2010) any real-world questions, including the relevant data, that they may have; problems which fit the workshop's goals might be discussed with the teachers during the Friday's afternoon exercise session.

Registration opened until January 9th:

<http://www.ch.embnet.org/CoursEMBnet/PagesSTATS10/Introduction.php>

For more information please contact Dr. Vassilios Ioannidis

[vassilios.ioannidis@isb-sib.ch](mailto:vassilios.ioannidis@isb-sib.ch)

#### 2) Computational Analysis of Ultra-High-Throughput (UHT) Sequencing Data

Research based on ultra-high-throughput (UHT) sequencing technologies

is to a large extent bioinformatics: The aims of the course are: (i)

UNDERSTANDING the biological questions addressed with these technologies, the nature of the data (Including noise and artifacts),

the current state-of-the-art algorithms to interpret the data, and the computational challenges in the near future. (ii) KNOWING the major

application areas of UHT sequencing, (iii) BEING ABLE to learn more from the corresponding scientific literature.

Program

UHT sequencing technologies, raw data management, base calling, de novo and homology-driven assembly of genomes, large-scale genotyping (SNP, CNV), ChiP-seq, transcription start site mapping, gene expression profiling. The topics will be covered by introductory

lectures, hands-on practicals, and research seminars by users of UHT sequencing technologies.

Registration opened until July 31st:

<http://www.ch.embnet.org/CoursEMBnet/PagesUHTS10/Introduction.php>

For more information please contact Dr. Vassilios Ioannidis

[vassilios.ioannidis@isb-sib.ch](mailto:vassilios.ioannidis@isb-sib.ch)

EMBnet in 2010

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As announced in March 2009, we confirm that our activities will be integrated into the Vital-IT group of the SIB and further developed in collaboration with other SIB groups. The EMBnet team won't be responsible for running those new portals, however the current web sites and services are maintained until the new sites will officially take over. You will be kept informed in due time about the new services.

To ensure a continuity of service, please fill in the general survey:

<http://www.ch.embnet.org/pages/survey09.html>

How to contact us ?

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Don't forget our official help desk email address:

[helpdesk@mail.ch.embnet.org](mailto:helpdesk@mail.ch.embnet.org)

When sending an email to this address you will automatically receive a ticket with a number. Your question will be answered by our team or by an expert in the field from the Swiss Institute of Bioinformatics.

With our best regards,

Laurent Falquet, Swiss EMBnet node manager  
and the Swiss EMBnet team members,  
Vassilios Ioannidis  
Sébastien Moretti

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EMBnet News reports developments and changes affecting the Swiss EMBnet node.

EMBnet News articles report on newservices, links added to the node's Web pages, changes affecting users of EMBOSS and other software packages, planned upgrades likely to affect services, etc.

Users of Swiss EMBnet services are strongly encouraged to subscribe, as this is our main mode of communication with them.

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